SEQUENCE LISTING

<110> Skeiky, Yasir
Reed, Steven
Alderson, Mark
Corixa Corporation

<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009050US

<140> US 09/597,796
<141> 2000-06-20

<150> US 09/056,556
<151> 1998-04-07

<150> US 09/223,040
<151> 1998-12-30

<150> WO PCT/US99/07717
<151> 1999-04-07

<150> US 09/287,849
<151> 1999-04-07

<150> US 60/158,338
<151> 1999-10-07

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<160> 30

<170> PatentIn Ver. 2.1

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<211> 588
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Ra35, N-terminus of MTB32A (TbRa35FL)

<220>
<221> CDS
<222> (1)..(588)
<223> Ra35

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<210> 2
<211> 195
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Ra35, N-terminus of MTB32A (TbRa35FL)

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35 40 45
Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
50 55 60
Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
65 70 75 80
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
85 90 95
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
100 105 110
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
115 120 125
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
130 135 140
Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
145 150 155 160
Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
165 170 175
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180 185 190
Ala Ala Ser
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<210> 3
<211> 1872
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB32A (TbRa35FL) cDNA

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<222> (1460)
<223> n = g, a, c or t

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<222> (1854)
<223> n = g, a, c or t

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<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB32A (TbRa35FL) protein

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35 40 45
Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
50 55 60
Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
65 70 75 80
Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
85 90 95
Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
100 105 110
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
115 120 125
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
130 135 140
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
145 150 155 160
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
165 170 175

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Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
        195                 200                 205
Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
    210                 215                 220
Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
225                 230                 235                 240
Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
                245                 250                 255
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
            260                 265                 270
Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
        275                 280                 285
Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
    290                 295                 300
Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
305                 310                 315                 320
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
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<210> 5
<211> 447
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTBRa12 C-terminus of MTB32A (Ra35FL)

<400> 5
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caccgttcat atcgggccta ccgccttcct cggcttgggt gttgtcgaca acaacggcaa 180
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cgcgcttaac gggcatcatc ccggtgacgt catctcggtg aactggcaaa ccaagtcggg 360
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ataccacccg ccggccggcc aattgga                                     447
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<210> 6
<211> 132
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTBRa12 C-terminus of MTB32A (Ra35FL)

<400> 6
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             20                  25                  30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
         35                  40                  45
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Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65                  70                  75                  80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
                 85                  90                  95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
            100                 105                 110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
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Gly Pro Pro Ala
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<210> 7
<211> 3058
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9) cDNA full-length

<400> 7

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<210> 8
<211> 391
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9) protein full-length

<400> 8

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        35                  40                  45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
    50                  55                  60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65                  70                  75                  80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
                85                  90                  95
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
            100                 105                 110
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
        115                 120                 125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
    130                 135                 140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
145                 150                 155                 160
Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
                165                 170                 175
Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
            180                 185                 190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
        195                 200                 205
Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
    210                 215                 220
Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
225                 230                 235                 240
Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
                245                 250                 255
Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
            260                 265                 270
Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
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305                 310                 315                 320
Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
                325                 330                 335
Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
            340                 345                 350
Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
        355                 360                 365
Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
    370                 375                 380
Pro His Ser Pro Ala Ala Gly
385                 390
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<210> 9
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion
protein TbH9-Ra35 (MTB59F)

<220>
<221> CDS
<222> (1)..(1791)
<223> MTB59F

<400> 9

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<210> 10
<211> 596
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein TbH9-Ra35 (MTB59F)

<400> 10

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        35                  40                  45
Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
    50                  55                  60
Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
65                  70                  75                  80
Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
                85                  90                  95
Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
            100                 105                 110
Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
        115                 120                 125
Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
    130                 135                 140
Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
145                 150                 155                 160
Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
                165                 170                 175
Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
            180                 185                 190
Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
        195                 200                 205
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    210                 215                 220
Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
225                 230                 235                 240
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
                245                 250                 255
Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
            260                 265                 270
Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr
        275                 280                 285
Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
    290                 295                 300
Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
305                 310                 315                 320
Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn
                325                 330                 335
Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
            340                 345                 350
Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
        355                 360                 365
Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg
    370                 375                 380
Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
385                 390                 395                 400
```

```
Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala
                405                 410                 415
Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val
            420                 425                 430
Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly
        435                 440                 445
Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His
    450                 455                 460
Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
465                 470                 475                 480
Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val
                485                 490                 495
Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile
            500                 505                 510
Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser
        515                 520                 525
Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
    530                 535                 540
Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu
545                 550                 555                 560
Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp
                565                 570                 575
Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
            580                 585                 590
Thr Ala Ala Ser
        595
```

<210> 11
<211> 2287
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein Ra12-TbH9-Ra35 (MTB72F)

<220>
<221> modified_base
<222> (30)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (33)
<223> n = g, a, c or t

<220>
<221> CDS
<222> (42)..(2231)
<223> MTB72F

<220>
<221> modified_base
<222> (2270)
<223> n = g, a, c or t

<400> 11
tctagaaata attttgttta ctttaagaan ganatataca tatgcatcac catcaccatc 60
acacggccgc gtccgataac ttccagctgt cccagggtgg gcagggattc gccattccga 120
tcgggcaggc gatggcgatc gcgggccaga tccgatcggg tgggggtca cccaccgttc 180

```
atatcgggcc taccgccttc ctcggcttgg gtgttgtcga caacaacggc aacggcgcac 240
gagtccaacg cgtggtcggg agcgctccgg cggcaagtct cggcatctcc accggcgacg 300
tgatcaccgc ggtcgacggc gctccgatca actcggccac cgcgatggcg gacgcgctta 360
acgggcatca tcccggtgac gtcatctcgg tgacctggca aaccaagtcg ggcggcacgc 420
gtacagggaa cgtgacattg gccgagggac ccccggccga attcatggtg gatttcgggg 480
cgttaccacc ggagatcaac tccgcgagga tgtacgccgg cccgggttcg gcctcgctgg 540
tggccgcggc tcagatgtgg gacagcgtgg cgagtgacct gttttcggcc gcgtcggcgt 600
ttcagtcggt ggtctggggt ctgacggtgg ggtcgtggat aggttcgtcg gcgggtctga 660
tggtggcggc ggcctcgccg tatgtggcgt ggatgagcgt caccgcgggg caggccgagc 720
tgaccgccgc ccaggtccgg gttgctgcgg cggcctacga gacggcgtat gggctgacgg 780
tgcccccgcc ggtgatcgcc gagaaccgtg ctgaactgat gattctgata gcgaccaacc 840
tcttggggca aaacaccccg gcgatcgcgg tcaacgaggc cgaatacggc gagatgtggg 900
cccaagacgc cgccgcgatg tttggctacg ccgcggcgac ggcgacggcg acggcgacgt 960
tgctgccgtt cgaggaggcg ccggagatga ccagcgcggg tgggctcctc gagcaggccg 1020
ccgcggtcga ggaggcctcc gacaccgccg cggcgaacca gttgatgaac aatgtgcccc 1080
aggcgctgca acagctggcc cagcccacgc agggcaccac gccttcttcc aagctgggtg 1140
gcctgtggaa gacggtctcg ccgcatcggt cgccgatcag caacatggtg tcgatggcca 1200
acaaccacat gtcgatgacc aactcgggtg tgtcgatgac caacaccttg agctcgatgt 1260
tgaagggctt tgctccggcg gcggcccgcc aggccgtgca aaccgcggcg caaaacgggg 1320
tccgggcgat gagctcgctg ggcagctcgc tgggttcttc gggtctgggc ggtggggtgg 1380
ccgccaactt gggtcgggcg gcctcggtcg gttcgttgtc ggtgccgcag gcctgggccg 1440
cggccaacca ggcagtcacc ccggcggcgc gggcgctgcc gctgaccagc ctgaccagcg 1500
ccgcggaaag agggcccggg cagatgctgg gcgggctgcc ggtggggcag atgggcgcca 1560
gggccggtgg tgggctcagt ggtgtgctgc gtgttccgcc gcgaccctat gtgatgccgc 1620
attctccggc agccggcgat atcgccccgc cggccttgtc gcaggaccgg ttcgccgact 1680
tccccgcgct gcccctcgac ccgtccgcga tggtcgccca agtggggcca caggtggtca 1740
acatcaacac caaactgggc tacaacaacg ccgtgggcgc cgggaccggc atcgtcatcg 1800
atcccaacgg tgtcgtgctg accaacaacc acgtgatcgc gggcgccacc gacatcaatg 1860
cgttcagcgt cggctccggc caaacctacg gcgtcgatgt ggtcgggtat gaccgcaccc 1920
aggatgtcgc ggtgctgcag ctgcgcggtg ccggtggcct gccgtcggcg gcgatcggtg 1980
gcggcgtcgc ggttggtgag cccgtcgtcg cgatgggcaa cagcggtggg cagggcggaa 2040
cgccccgtgc ggtgcctggc agggtggtcg cgctcggcca aaccgtgcag gcgtcggatt 2100
cgctgaccgg tgccgaagag acattgaacg ggttgatcca gttcgatgcc gcgatccagc 2160
ccggtgattc gggcgggccc gtcgtcaacg gcctaggaca ggtggtcggt atgaacacgg 2220
ccgcgtccta ggatatccat cacactggcg gccgctcgag cagatccggn tgtaacaaag 2280
cccgaaa                                                          2287
```

<210> 12
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein Ra12-TbH9-Ra35 (MTB72F)

<400> 12

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Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
  1               5                  10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
        35                  40                  45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
    50                  55                  60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65                  70                  75                  80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
                85                  90                  95
```

```
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
                100                 105                 110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
            115                 120                 125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
        130                 135                 140
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
145                 150                 155                 160
Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
                165                 170                 175
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
            180                 185                 190
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
        195                 200                 205
Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
    210                 215                 220
Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu
225                 230                 235                 240
Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
                245                 250                 255
Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
            260                 265                 270
Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
        275                 280                 285
Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
    290                 295                 300
Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
305                 310                 315                 320
Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
                325                 330                 335
Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
            340                 345                 350
Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
        355                 360                 365
Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
    370                 375                 380
Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
385                 390                 395                 400
Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Arg
                405                 410                 415
Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
            420                 425                 430
Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
        435                 440                 445
Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
    450                 455                 460
Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
465                 470                 475                 480
Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
                485                 490                 495
Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu
            500                 505                 510
Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
        515                 520                 525
Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
    530                 535                 540
Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
545                 550                 555                 560
Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
                565                 570                 575
```

```
Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
            580                 585                 590
Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
        595                 600                 605
Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
    610                 615                 620
Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
625                 630                 635                 640
Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
                645                 650                 655
Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
            660                 665                 670
Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
        675                 680                 685
Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
    690                 695                 700
Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705                 710                 715                 720
Val Val Gly Met Asn Thr Ala Ala Ser
                725
```

<210> 13
<211> 500
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb8.4 (DPV)

<400> 13
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cgtggcaatg tcgttgaccg tcggggccgg ggtcgcctcc gcagatcccg tggacgcggt 60
cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
ggctgccgca cagttcaacg cctcaccggt ggcgcagtcc tatttgcgca atttcctcgc 180
cgcaccgcca cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cgggggcggc 240
acagtacatc ggccttgtcg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300
gggccccatc ccgcgacccg gcatcgtcgc cggggctagg ccagattgcc ccgctcctca 360
acgggccgca tcccgcgacc cggcatcgtc gccggggcta ggccagattg ccccgctcct 420
caacgggccg catctcgtgc cgaattcctg cagcccgggg gatccactag ttctagagcg 480
gccgccaccg cggtggagct                                            500
```

<210> 14
<211> 96
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb8.4 (DPV)

<400> 14
```
Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
  1               5                  10                  15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
             20                  25                  30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
         35                  40                  45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
     50                  55                  60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
 65                  70                  75                  80
```

```
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
                85                  90                  95


<210> 15
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 15
tggattccga tagcggtttc ggcccctcga cgggcgacca cggcgcgcag gcctccgaac 60
gggggccgg gacgctggga ttcgccggga ccgcaaccaa agaacgccgg gtccgggcgg 120
tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatggtgc 180
cggggacctg ggagcagggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggacccgtac 300
gggtcgaaag gagagatgtt atgagccttt tggatgctca tatcccacag ttggtggcct 360
cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cacgatcggt caggccgagc 420
aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcggcg tttcaggccg 480
cccatgcccg gtttgtggcg gcggccgcca aagtcaacac cttgttggat gtcgcgcagg 540
cgaatctggg tgaggccgcc ggtacctatg tggccgccga tgctg                  585


<210> 16
<211> 97
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 16
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
  1               5                  10                  15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
             20                  25                  30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
         35                  40                  45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
     50                  55                  60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65                  70                  75                  80
Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
                85                  90                  95
Phe


<210> 17
<211> 1742
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.9A (MTI, MTI-A)

<220>
<221> modified_base
<222> (1)..(1742)
<223> n = g, a, c or t
```

<400> 17
ccgctctctt tcaacgtcat aagttcggtg ggccagtcgg ccgcgcgtgc atatggcacc 60
aataacgcgt gtcccatgga tacccggacc gcacgacggt agagcggatc agcgcagccg 120
gtgccgaaca ctaccgcgtc cacgctcagc cctgccgcgt tgcggaagat cgagcccagg 180
ttctcatggt cgttaacgcc ttccaacact gcgacggtgc gcgccccggc gaccacctga 240
gcaacgctcg gctccggcac ccggcgcgcg gctgccaaca ccccacgatt gagatggaag 300
ccgatcaccc gtgccatgac atcagccgac gctcgatagt acggcgcgcc gacaccggcc 360
agatcatcct tgagctcggc cagccggcgg tcggtgccga acagcgccag cggcgtgaac 420
cgtgaggcca gcatgcgctg caccaccagc acaccctcgg cgatcaccaa cgccttgccg 480
gtcggcagat cgggacnacn gtcgatgctg ttcaggtcac ggaaatcgtc gagccgtggg 540
tcgtcgggat cgcagacgtc ctgaacatcg aggccgtcgg ggtgctgggc acaacggcct 600
tcggtcacgg gctttcgtcg accagagcca gcatcagatc ggcggcgctg cgcaggatgt 660
cacgctcgct gcggttcagc gtcgcgagcc gctcagccag ccactcttgc agagagccgt 720
tgctgggatt aattgggaga ggaagacagc atgtcgttcg tgaccacaca gccggaagcc 780
ctggcagctg cggcggcgaa cctacagggt attggcacga caatgaacgc ccagaacgcg 840
gccgcggctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgctg 900
accgcggctc agtttgctgc gcacgcgcag atgtaccaaa cggtcagcgc ccaggccgcg 960
gccattcacg aaatgttcgt gaacacgctg gtggccagtt ctggctcata cgcggccacc 1020
gaggcggcca acgcagccgc tgccggctga acgggctcgc acgaacctgc tgaaggagag 1080
ggggaacatc cggagttctc gggtcagggg ttgcgccagc gcccagccga ttcagntatc 1140
ggcgtccata acagcagacg atctaggcat tcagtactaa ggagacaggc aacatggcct 1200
cacgttttat gacggatccg catgcgatgc gggacatggc gggccgtttt gaggtgcacg 1260
cccagacggt ggaggacgag gctcgccgga tgtgggcgtc cgcgcaaaac atttccggtg 1320
cgggctggag tggcatggcc gaggcgacct cgctagacac catgacctag atgaatcagg 1380
cgtttcgcaa catcgtgaac atgctgcacg gggtgcgtga cgggctggtt cgcgacgcca 1440
acaantacga acagcaagag caggcctccc agcagatcct gagcagntag cgccgaaagc 1500
cacagctgng tacgntttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
cggggacgtc gacgctcatg gcgccatgat ccgcgctcag gcggcgtcgc ttgaggcgga 1620
gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac ttttggggcg gcgccggttc 1680
ggtggcttgc caggagttca ttacccagtt gggccgtaac ttccaggtga tctacgagca 1740
gg 1742

<210> 18
<211> 94
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.9A (MTI, MTI-A)

<400> 18
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
20 25 30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35 40 45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

<210> 19
<211> 1200
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB40 (HTCC#1) cDNA

<400> 19
caggcatgag cagagcgttc atcatcgatc caacgatcag tgccattgac ggcttgtacg 60
accttctggg gattggaata cccaaccaag ggggtatcct ttactcctca ctagagtact 120
tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180
ccgcggacaa atacgccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcggtc cagacgaccc 300
gcgacatcct ggagggcgcc aagaaaggtc tcgagttcgt gcgcccggtg gctgtggacc 360
tgacctacat cccggtcgtc gggcacgccc tatcggccgc cttccaggcg ccgttttgcg 420
cgggcgcgat ggccgtagtg ggcggcgcgc ttgcctactt ggtcgtgaaa acgctgatca 480
acgcgactca actcctcaaa ttgcttgcca aattggcgga gttggtcgcg gccgccattg 540
cggacatcat ttcggatgtg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
tcatcacaaa cgcgctcaac ggcctgaaag agctttggga caagctcacg gggtgggtga 660
ccggactgtt ctctcgaggg tggtcgaacc tggagtcctt ctttgcgggc gtccccggct 720
tgaccggcgc gaccagcggc ttgtcgcaag tgactggctt gttcggtgcg gccggtctgt 780
ccgcatcgtc gggcttggct cacgcggata gcctggcgag ctcagccagc ttgcccgccc 840
tggccggcat tgggggcggg tccggttttg ggggcttgcc gagcctggct caggtccatg 900
ccgcctcaac tcggcaggcg ctacggcccc gagctgatgg cccggtcggc gccgctgccg 960
agcaggtcgg cgggcagtcg cagctggtct ccgcgcaggg ttcccaaggt atgggcggac 1020
ccgtaggcat gggcggcatg cacccctctt cgggggcgtc gaaagggacg acgacgaaga 1080
agtactcgga aggcgcggcg gcgggcactg aagacgccga gcgcgcgcca gtcgaagctg 1140
acgcgggcgg tgggcaaaag gtgctggtac gaaacgtcgt ctaacggcat ggcgagccaa 1200

<210> 20
<211> 392
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB40 (HTCC#1)

<400> 20
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100 105 110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115 120 125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130 135 140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145 150 155 160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165 170 175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180 185 190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195 200 205

```
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
    210                 215                 220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225                 230                 235                 240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
                245                 250                 255
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
            260                 265                 270
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
        275                 280                 285
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
    290                 295                 300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305                 310                 315                 320
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
                325                 330                 335
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
            340                 345                 350
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
        355                 360                 365
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
    370                 375                 380
Lys Val Leu Val Arg Asn Val Val
385                 390
```

<210> 21
<211> 1441
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2)

<400> 21

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gaggttgctg gcaatggatt tcgggctttt acctccggaa gtgaattcaa gccgaatgta 60
ttccggtccg gggccggagt cgatgctagc cgccgcggcc gcctgggacg gtgtggccgc 120
ggagttgact tccgccgcgg tctcgtatgg atcggtggtg tcgacgctga tcgttgagcc 180
gtggatgggg ccggcggcgg ccgcgatggc ggccgcggca acgccgtatg tggggtggct 240
ggccgccacg gcggcgctgg cgaaggagac ggccacacag gcgagggcag cggcggaagc 300
gtttgggacg gcgttcgcga tgacggtgcc accatccctc gtcgcggcca accgcagccg 360
gttgatgtcg ctggtcgcgg cgaacattct ggggcaaaac agtgcggcga tcgcggctac 420
ccaggccgag tatgccgaaa tgtgggccca agacgctgcc gtgatgtaca gctatgaggg 480
ggcatctgcg gccgcgtcgg cgttgccgcc gttcactcca cccgtgcaag gcaccggccc 540
ggccgggccc gcggccgcag ccgcggcgac ccaagccgcc ggtgcgggcg ccgttgcgga 600
tgcacaggcg acactggccc agctgccccc ggggatcctg agcgacattc tgtccgcatt 660
ggccgccaac gctgatccgc tgacatcggg actgttgggg atcgcgtcga ccctcaaccc 720
gcaagtcgga tccgctcagc cgatagtgat ccccaccccg ataggggaat tggacgtgat 780
cgcgctctac attgcatcca tcgcgaccgg cagcattgcg ctcgcgatca cgaacacggc 840
cagaccctgg cacatcggcc tatacgggaa cgccggcggg ctgggaccga cgcagggcca 900
tccactgagt tcggcgaccg acgagccgga gccgcactgg ggccccttcg ggggcgcggc 960
gccggtgtcc gcgggcgtcg gccacgcagc attagtcgga gcgttgtcgg tgccgcacag 1020
ctggaccacg gccgccccgg agatccagct cgccgttcag gcaacaccca ccttcagctc 1080
cagcgccggc gccgacccga cggccctaaa cgggatgccg gcaggcctgc tcagcgggat 1140
ggctttggcg agcctggccg cacgcggcac gacgggcggt ggcggcaccc gtagcggcac 1200
cagcactgac ggccaagagg acggccgcaa acccccggta gttgtgatta gagagcagcc 1260
gccgcccgga aacccccccgc ggtaaaagtc cggcaaccgt tcgtcgccgc gcggaaaatg 1320
cctggtgagc gtggctatcc gacgggccgt tcacaccgct tgtagtagcg tacggctatg 1380
gacgacggtg tctggattct cggcggctat cagagcgatt ttgctcgcaa cctcagcaaa 1440
g                                                                   1441
```

<210> 22
<211> 423
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2)

<400> 22
Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
1 5 10 15
Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
20 25 30
Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
35 40 45
Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
50 55 60
Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
65 70 75 80
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
85 90 95
Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
100 105 110
Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
115 120 125
Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
130 135 140
Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
145 150 155 160
Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
165 170 175
Ala Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
180 185 190
Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
195 200 205
Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
210 215 220
Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
225 230 235 240
Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
245 250 255
Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
260 265 270
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
275 280 285
Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
290 295 300
Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
305 310 315 320
Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
325 330 335
Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
340 345 350
Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
355 360 365
Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
370 375 380
Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
385 390 395 400
Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
405 410 415

Pro Pro Gly Asn Pro Pro Arg
420

<210> 23
<211> 154
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 23
atgacagagc agcagtggaa tttcgcgggt atcgaggccg cggcaagcgc aatccaggga 60
aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120
gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 24
<211> 51
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 24
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45
Glu Ala Tyr
50

<210> 25
<211> 851
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9) cDNA

<400> 25
ctgcagggtg gcgtggatga gcgtcaccgc ggggcaggcc gagctgaccg ccgcccaggt 60
ccgggttgct gcggcggcct acgagacggc gtatgggctg acggtgcccc cgccggtgat 120
cgccgagaac cgtgctgaac tgatgattct gatagcgacc aacctcttgg ggcaaaacac 180
cccggcgatc gcggtcaacg aggccgaata cggcgagatg tgggcccaag acgccgccgc 240
gatgtttggc tacgccgcgg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300
ggcgccggag atgaccagcg cgggtgggct cctcgagcag gccgccgcgg tcgaggaggc 360
ctccgacacc gccgcggcga accagttgat gaacaatgtg ccccaggcgc tgaaacagtt 420
ggcccagccc acgcagggca ccacgccttc ttccaagctg ggtggcctgt ggaagacggt 480
ctcgccgcat cggtcgccga tcagcaacat ggtgtcgatg gccaacaacc acatgtcgat 540
gaccaactcg ggtgtgtcga tgaccaacac cttgagctcg atgttgaagg gctttgctcc 600
ggcggcggcc gcccaggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660
gctgggcagc tcgctgggtt cttcgggtct gggcggtggg gtggccgcca acttgggtcg 720
ggcggcctcg gtacggtatg gtcaccggga tggcggaaaa tatgcanagt ctggtcggcg 780
gaacggtggt ccggcgtaag gtttaccccc gttttctgga tgcggtgaac ttcgtcaacg 840
gaaacagtta c 851

<210> 26
<211> 263
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9)

<400> 26
Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1 5 10 15
Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20 25 30
Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35 40 45
Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50 55 60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65 70 75 80
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85 90 95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100 105 110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115 120 125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
130 135 140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145 150 155 160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165 170 175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180 185 190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala
195 200 205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
210 215 220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
225 230 235 240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
245 250 255
Arg Arg Asn Gly Gly Pro Ala
260

<210> 27
<211> 474
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<221> CDS
<222> (16)..(450)
<223> alpha-crystalline antigen

<400> 27
attaggaggc atcaa atg gcc acc acc ctt ccc gtt cag cgc cac ccg cgg 51
Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg
1 5 10

```
tcc ctc ttc ccc gag ttt tct gag ctg ttc gcg gcc ttc ccg tca ttc    99
Ser Leu Phe Pro Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe
          15                  20                  25

gcc gga ctc cgg ccc acc ttc gac acc cgg ttg atg cgg ctg gaa gac   147
Ala Gly Leu Arg Pro Thr Phe Asp Thr Arg Leu Met Arg Leu Glu Asp
      30                  35                  40

gag atg aaa gag ggg cgc tac gag gta cgc gcg gag ctt ccc ggg gtc   195
Glu Met Lys Glu Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val
 45                  50                  55                  60

gac ccc gac aag gac gtc gac att atg gtc cgc gat ggt cag ctg acc   243
Asp Pro Asp Lys Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr
                 65                  70                  75

atc aag gcc gag cgc acc gag cag aag gac ttc gac ggt cgc tcg gaa   291
Ile Lys Ala Glu Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu
             80                  85                  90

ttc gcg tac ggt tcc ttc gtt cgc acg gtg tcg ctg ccg gta ggt gct   339
Phe Ala Tyr Gly Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala
          95                  100                 105

gac gag gac gac att aag gcc acc tac gac aag ggc att ctt act gtg   387
Asp Glu Asp Asp Ile Lys Ala Thr Tyr Asp Lys Gly Ile Leu Thr Val
     110                 115                 120

tcg gtg gcg gtt tcg gaa ggg aag cca acc gaa aag cac att cag atc   435
Ser Val Ala Val Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile
125                 130                 135                 140

cgg tcc acc aac tga ccactgggtc cgtgctgatg accg                   474
Arg Ser Thr Asn
                145
```

<210> 28
<211> 144
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> alpha-crystalline antigen

<400> 28

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Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg Ser Leu Phe Pro
  1               5                  10                  15
Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe Ala Gly Leu Arg
             20                  25                  30
Pro Thr Phe Asp Thr Arg Leu Met Arg Leu Glu Asp Glu Met Lys Glu
         35                  40                  45
Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val Asp Pro Asp Lys
     50                  55                  60
Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr Ile Lys Ala Glu
 65                  70                  75                  80
Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu Phe Ala Tyr Gly
                 85                  90                  95
Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala Asp Glu Asp Asp
            100                 105                 110
```

```
Ile Lys Ala Thr Tyr Asp Lys Gly Ile Leu Thr Val Ser Val Ala Val
        115                 120                 125
Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile Arg Ser Thr Asn
    130                 135                 140


<210> 29
<211> 1211
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<221> CDS
<222> (150)..(1172)
<223> 85 complex antigen (MTB85 complex antigen)

<400> 29
aggtgtccgg gccgacgctg aatcgttagc caaccgcgat ctcgcgctgc ggccacgaca 60

ttcgaactga gcgtcctcgg tgtgtttcac tcgcccagaa cagattcgac cgcgtcgtgc 120

gcagatgaga gttgggattg gtagtagct atg acg ttc ttc gaa cag gtg cga  173
                                Met Thr Phe Phe Glu Gln Val Arg
                                  1               5

agg ttg cgg agc gca gcg aca acc ctg ccg cgc cgc gtg gct atc gcg  221
Arg Leu Arg Ser Ala Ala Thr Thr Leu Pro Arg Arg Val Ala Ile Ala
     10                  15                  20

gct atg ggg gct gtc ctg gtt tac ggt ctg gtc ggt acc ttc ggc ggg  269
Ala Met Gly Ala Val Leu Val Tyr Gly Leu Val Gly Thr Phe Gly Gly
 25                  30                  35                  40

ccg gcc acc gcg ggc gca ttc tct agg ccc ggt ctt cca gtg gaa tat  317
Pro Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val Glu Tyr
                 45                  50                  55

ctg cag gtg cca tcc gcg tcg atg ggc cgc gac atc aag gtc cag ttc  365
Leu Gln Val Pro Ser Ala Ser Met Gly Arg Asp Ile Lys Val Gln Phe
             60                  65                  70

cag ggc ggc gga ccg cac gcg gtc tac ctg ctc gac ggt ctg cgg gcc  413
Gln Gly Gly Gly Pro His Ala Val Tyr Leu Leu Asp Gly Leu Arg Ala
         75                  80                  85

cag gat gac tac aac ggc tgg gac atc aac acc ccg gcc ttc gag gag  461
Gln Asp Asp Tyr Asn Gly Trp Asp Ile Asn Thr Pro Ala Phe Glu Glu
     90                  95                  100

tac tac cag tca ggg ttg tcg gtg atc atg ccc gtg ggc ggc caa tcc  509
Tyr Tyr Gln Ser Gly Leu Ser Val Ile Met Pro Val Gly Gly Gln Ser
105                 110                 115                 120

agt ttc tac acc gac tgg tat cag ccc tcg cag agc aac ggc cag aac  557
Ser Phe Tyr Thr Asp Trp Tyr Gln Pro Ser Gln Ser Asn Gly Gln Asn
                125                 130                 135

tac acc tac aag tgg gag acc ttc ctt acc aga gag atg ccc gcc tgg  605
Tyr Thr Tyr Lys Trp Glu Thr Phe Leu Thr Arg Glu Met Pro Ala Trp
            140                 145                 150
```

```
cta cag gcc aac aag ggc gtg tcc ccg aca ggc aac gcg gcg gtg ggt   653
Leu Gln Ala Asn Lys Gly Val Ser Pro Thr Gly Asn Ala Ala Val Gly
        155                 160                 165

ctt tcg atg tcg ggc ggt tcc gcg ctg atc ctg gcc gcg tac tac ccg   701
Leu Ser Met Ser Gly Gly Ser Ala Leu Ile Leu Ala Ala Tyr Tyr Pro
    170                 175                 180

cag cag ttc ccg tac gcc gcg tcg ttg tcg ggc ttc ctc aac ccg tcc   749
Gln Gln Phe Pro Tyr Ala Ala Ser Leu Ser Gly Phe Leu Asn Pro Ser
185                 190                 195                 200

gag ggc tgg tgg ccg acg ctg atc ggc ctg gcg atg aac gac tcg ggc   797
Glu Gly Trp Trp Pro Thr Leu Ile Gly Leu Ala Met Asn Asp Ser Gly
                205                 210                 215

ggt tac aac gcc aac agc atg tgg ggt ccg tcc agc gac ccg gcc tgg   845
Gly Tyr Asn Ala Asn Ser Met Trp Gly Pro Ser Ser Asp Pro Ala Trp
            220                 225                 230

aag cgc aac gac cca atg gtt cag att ccc cgc ctg gtc gcc aac aac   893
Lys Arg Asn Asp Pro Met Val Gln Ile Pro Arg Leu Val Ala Asn Asn
        235                 240                 245

acc cgg atc tgg gtg tac tgc ggt aac ggc aca ccc agc gac ctc ggc   941
Thr Arg Ile Trp Val Tyr Cys Gly Asn Gly Thr Pro Ser Asp Leu Gly
    250                 255                 260

ggc gac aac ata ccg gcg aag ttc ctg gaa ggc ctc acc ctg cgc acc   989
Gly Asp Asn Ile Pro Ala Lys Phe Leu Glu Gly Leu Thr Leu Arg Thr
265                 270                 275                 280

aac cag acc ttc cgg gac acc tac gcg gcc gac ggt gga cgc aac ggg   1037
Asn Gln Thr Phe Arg Asp Thr Tyr Ala Ala Asp Gly Gly Arg Asn Gly
                285                 290                 295

gtg ttt aac ttc ccg ccc aac gga aca cac tcg tgg ccc tac tgg aac   1085
Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp Pro Tyr Trp Asn
            300                 305                 310

gag cag ctg gtc gcc atg aag gcc gat atc cag cat gtg ctc aac ggc   1133
Glu Gln Leu Val Ala Met Lys Ala Asp Ile Gln His Val Leu Asn Gly
        315                 320                 325

gcg aca ccc ccg gcc gcc cct gct gcg ccg gcc gcc tga gccagcaagc    1182
Ala Thr Pro Pro Ala Ala Pro Ala Ala Pro Ala Ala
    330                 335                 340

cagcatcggc agcagcgcaa cggccagcg                                  1211
```

<210> 30
<211> 340
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> 85 complex antigen (MTB85 complex antigen)

<400> 30

```
Met Thr Phe Phe Glu Gln Val Arg Arg Leu Arg Ser Ala Ala Thr Thr
  1               5                  10                  15
Leu Pro Arg Arg Val Ala Ile Ala Ala Met Gly Ala Val Leu Val Tyr
            20                  25                  30
Gly Leu Val Gly Thr Phe Gly Gly Pro Ala Thr Ala Gly Ala Phe Ser
        35                  40                  45
Arg Pro Gly Leu Pro Val Glu Tyr Leu Gln Val Pro Ser Ala Ser Met
    50                  55                  60
Gly Arg Asp Ile Lys Val Gln Phe Gln Gly Gly Gly Pro His Ala Val
65                  70                  75                  80
Tyr Leu Leu Asp Gly Leu Arg Ala Gln Asp Asp Tyr Asn Gly Trp Asp
                85                  90                  95
Ile Asn Thr Pro Ala Phe Glu Glu Tyr Tyr Gln Ser Gly Leu Ser Val
            100                 105                 110
Ile Met Pro Val Gly Gly Gln Ser Ser Phe Tyr Thr Asp Trp Tyr Gln
        115                 120                 125
Pro Ser Gln Ser Asn Gly Gln Asn Tyr Thr Tyr Lys Trp Glu Thr Phe
    130                 135                 140
Leu Thr Arg Glu Met Pro Ala Trp Leu Gln Ala Asn Lys Gly Val Ser
145                 150                 155                 160
Pro Thr Gly Asn Ala Ala Val Gly Leu Ser Met Ser Gly Gly Ser Ala
                165                 170                 175
Leu Ile Leu Ala Ala Tyr Tyr Pro Gln Gln Phe Pro Tyr Ala Ala Ser
            180                 185                 190
Leu Ser Gly Phe Leu Asn Pro Ser Glu Gly Trp Trp Pro Thr Leu Ile
        195                 200                 205
Gly Leu Ala Met Asn Asp Ser Gly Gly Tyr Asn Ala Asn Ser Met Trp
    210                 215                 220
Gly Pro Ser Ser Asp Pro Ala Trp Lys Arg Asn Asp Pro Met Val Gln
225                 230                 235                 240
Ile Pro Arg Leu Val Ala Asn Asn Thr Arg Ile Trp Val Tyr Cys Gly
                245                 250                 255
Asn Gly Thr Pro Ser Asp Leu Gly Gly Asp Asn Ile Pro Ala Lys Phe
            260                 265                 270
Leu Glu Gly Leu Thr Leu Arg Thr Asn Gln Thr Phe Arg Asp Thr Tyr
        275                 280                 285
Ala Ala Asp Gly Gly Arg Asn Gly Val Phe Asn Phe Pro Pro Asn Gly
    290                 295                 300
Thr His Ser Trp Pro Tyr Trp Asn Glu Gln Leu Val Ala Met Lys Ala
305                 310                 315                 320
Asp Ile Gln His Val Leu Asn Gly Ala Thr Pro Pro Ala Ala Pro Ala
                325                 330                 335
Ala Pro Ala Ala
            340
```